



## SEQUENCE LISTING

&lt;110&gt; GLUCKSMANN, MARIA ALEXANDRA

<120> 93870, A HUMAN G-PROTEIN COUPLED  
RECEPTOR AND USES THEREFOR

&lt;130&gt; MPI2001-021P1RCP1 (M)

&lt;140&gt; 10/085,233

&lt;141&gt; 2002-02-28

&lt;150&gt; 60/272,677

&lt;151&gt; 2001-03-01

&lt;160&gt; 6

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 1684

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (147)...(1085)

<223> n at position 1384 can be any  
nucleotide

&lt;400&gt; 1

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tggaaagttgt agactggata agagatgctc agctaaggga gttcctggat ggcctttaga 120  
ttgatacacc aatcctctga aattgc atg caa aaa tgt gac ttc cca agt atg 173  
Met Gln Lys Cys Asp Phe Pro Ser Met  
1 5

cct ggc cac aat acc tcc agg aat tcc tct tgc gat cct ata gtg aca 221  
Pro Gly His Asn Thr Ser Arg Asn Ser Ser Cys Asp Pro Ile Val Thr  
10 15 20 25

ccc cac tta atc agc ctc tac ttc ata gtg ctt att ggc ggg ctg gtg 269  
Pro His Leu Ile Ser Leu Tyr Phe Ile Val Leu Ile Gly Gly Leu Val  
30 35 40

ggt gtc att tcc att ctt ttc ctc ctg gtg aaa atg aac acc cgg tca 317  
Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys Met Asn Thr Arg Ser  
45 50 55

gtg acc acc atg gcg gtc att aac ttg gtg gtg gtc cac agc gtt ttt 365  
Val Thr Thr Met Ala Val Ile Asn Leu Val Val His Ser Val Phe  
60 65 70

ctg ctg aca gtg cca ttt cgc ttg acc tac ctc atc aag aag act tgg 413  
Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu Ile Lys Lys Thr Trp  
75 80 85

atg ttt ggg ctg ccc ttc tgc aaa ttt gtg agt gcc atg ctg cac atc 461  
Met Phe Gly Leu Pro Phe Cys Lys Phe Val Ser Ala Met Leu His Ile  
90 95 100 105

cac atg tac ctc acg ttc cta ttc tat gtg gtg atc ctg gtc acc aga 509  
His Met Tyr Leu Thr Phe Leu Phe Tyr Val Val Ile Leu Val Thr Arg  
110 115 120

tac ctc atc ttc ttc aag tgc aaa gac aaa gtg gaa ttc tac aga aaa	557
Tyr Leu Ile Phe Phe Lys Cys Lys Asp Lys Val Glu Phe Tyr Arg Lys	
125 130 135	
ctg cat gct gtg gct gcc agt gct ggc atg tgg acg ctg gtg att gtc	605
Leu His Ala Val Ala Ala Ser Ala Gly Met Trp Thr Leu Val Ile Val	
140 145 150	
att gtg gta ccc ctg gtt gtc tcc cgg tat gga atc cat gag gaa tac	653
Ile Val Val Pro Leu Val Val Ser Arg Tyr Gly Ile His Glu Glu Tyr	
155 160 165	
aat gag gag cac tgt ttt aaa ttt cac aaa gag ctt gct tac aca tat	701
Asn Glu Glu His Cys Phe Lys Phe His Lys Glu Leu Ala Tyr Thr Tyr	
170 175 180 185	
gtg aaa atc atc aac tat atg ata gtc att ttt gtc ata gcc gtt gct	749
Val Lys Ile Ile Asn Tyr Met Ile Val Ile Phe Val Ile Ala Val Ala	
190 195 200	
gtg att ctg ttg gtc ttc cag gtc ttc atc att atg ttg atg gtg cag	797
Val Ile Leu Leu Val Phe Gln Val Phe Ile Ile Met Leu Met Val Gln	
205 210 215	
aag cta cgc cac tct tta cta tcc cac cag gag ttc tgg gct cag ctg	845
Lys Leu Arg His Ser Leu Leu Ser His Gln Glu Phe Trp Ala Gln Leu	
220 225 230	
aaa aac cta ttt ttt ata ggg gtc atc ctt gtt tgt ttc ctt ccc tac	893
Lys Asn Leu Phe Phe Ile Gly Val Ile Leu Val Cys Phe Leu Pro Tyr	
235 240 245	
cag ttc ttt agg atc tat tac ttg aat gtt gtg acg cat tcc aat gcc	941
Gln Phe Phe Arg Ile Tyr Tyr Leu Asn Val Val Thr His Ser Asn Ala	
250 255 260 265	
tgt agc agc aag gtt gca ttt tat aac gaa atc ttc ttg agt gta aca	989
Cys Ser Ser Lys Val Ala Phe Tyr Asn Glu Ile Phe Leu Ser Val Thr	
270 275 280	
gca att agc tgc tat gat ttg ctt ctc ttt gtc ttt ggg gga agc cat	1037
Ala Ile Ser Cys Tyr Asp Leu Leu Leu Phe Val Phe Gly Gly Ser His	
285 290 295	
tgg ttt aag caa aag ata att ggc tta tgg aat tgt gtt ttg tgc cgt	1085
Trp Phe Lys Gln Lys Ile Ile Gly Leu Trp Asn Cys Val Leu Cys Arg	
300 305 310	
tagccacaaa ctacagtatt catatggct tcctttat tggaaataaa atgggtata	1145
gggaggtaag aatggtattt cattacttga tcaaaaccat gccttgatgt accaaaaaca	1205
aaaggactat aaaatgcaag agccctcatt gtatcctta tggatccct cccatctctg	1265
agtatggcc gtacaaagac cagtgttgtt gaatccacct ggagttgcaa tattacatta	1325
tttccagta cagaatgtct gtgtggccca tgaaagcaac ataggttta agagtttta	1385
gagtttcatt agtcattct aagttcctct gtttgaagca tggctcttta ggtttggac	1445
tgaactcaga ccttttagttc ttttcatccc acttccat aggttaagtaa attctggcca	1505
ccacccagct ccaaagacac aaactctcct tcgctaacca gtttagatgt cccattcatc	1565
tcatgccctg ataaaaactg ataaggggag agaatgtta aaaattttc taggtatca	1625
taactctggt aggaagtcat ctgtctagac tcgagcaagc ttatgcatgc atgcggccg	1684

<210> 2  
<211> 313  
<212> PRT  
<213> Homo sapiens

<400> 2  
Met Gln Lys Cys Asp Phe Pro Ser Met Pro Gly His Asn Thr Ser Arg  
1 5 10 15  
Asn Ser Ser Cys Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr  
20 25 30

Phe Ile Val Leu Ile Gly Gly Leu Val Gly Val Ile Ser Ile Leu Phe  
     35                 40                 45  
 Leu Leu Val Lys Met Asn Thr Arg Ser Val Thr Thr Met Ala Val Ile  
     50                 55                 60  
 Asn Leu Val Val Val His Ser Val Phe Leu Leu Thr Val Pro Phe Arg  
     65                 70                 75                 80  
 Leu Thr Tyr Leu Ile Lys Lys Thr Trp Met Phe Gly Leu Pro Phe Cys  
     85                 90                 95  
 Lys Phe Val Ser Ala Met Leu His Ile His Met Tyr Leu Thr Phe Leu  
     100                105                110  
 Phe Tyr Val Val Ile Leu Val Thr Arg Tyr Leu Ile Phe Phe Lys Cys  
     115                120                125  
 Lys Asp Lys Val Glu Phe Tyr Arg Lys Leu His Ala Val Ala Ala Ser  
     130                135                140  
 Ala Gly Met Trp Thr Leu Val Ile Val Ile Val Val Pro Leu Val Val  
     145                150                155                160  
 Ser Arg Tyr Gly Ile His Glu Glu Tyr Asn Glu Glu His Cys Phe Lys  
     165                170                175  
 Phe His Lys Glu Leu Ala Tyr Thr Tyr Val Lys Ile Ile Asn Tyr Met  
     180                185                190  
 Ile Val Ile Phe Val Ile Ala Val Ala Val Ile Leu Leu Val Phe Gln  
     195                200                205  
 Val Phe Ile Ile Met Leu Met Val Gln Lys Leu Arg His Ser Leu Leu  
     210                215                220  
 Ser His Gln Glu Phe Trp Ala Gln Leu Lys Asn Leu Phe Phe Ile Gly  
     225                230                235                240  
 Val Ile Leu Val Cys Phe Leu Pro Tyr Gln Phe Phe Arg Ile Tyr Tyr  
     245                250                255  
 Leu Asn Val Val Thr His Ser Asn Ala Cys Ser Ser Lys Val Ala Phe  
     260                265                270  
 Tyr Asn Glu Ile Phe Leu Ser Val Thr Ala Ile Ser Cys Tyr Asp Leu  
     275                280                285  
 Leu Leu Phe Val Phe Gly Gly Ser His Trp Phe Lys Gln Lys Ile Ile  
     290                295                300  
 Gly Leu Trp Asn Cys Val Leu Cys Arg  
     305                310

<210> 3  
 <211> 939  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(939)

<400> 3  
 atg caa aaa tgt gac ttc cca agt atg cct ggc cac aat acc tcc agg      48  
 Met Gln Lys Cys Asp Phe Pro Ser Met Pro Gly His Asn Thr Ser Arg  
     1              5                 10                 15  
 aat tcc tct tgc gat cct ata gtg aca ccc cac tta atc agc ctc tac      96  
 Asn Ser Ser Cys Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr  
     20             25                 30  
 ttc ata gtg ctt att ggc ggg ctg gtg ggt gtc att tcc att ctt ttc      144  
 Phe Ile Val Leu Ile Gly Gly Leu Val Gly Val Ile Ser Ile Leu Phe  
     35             40                 45  
 ctc ctg gtg aaa atg aac acc cgg tca gtg acc acc atg gcg gtc att      192  
 Leu Leu Val Lys Met Asn Thr Arg Ser Val Thr Thr Met Ala Val Ile  
     50             55                 60  
 aac ttg gtg gtg gtc cac agc gtt ttt ctg ctg aca gtg cca ttt cgc      240  
 Asn Leu Val Val His Ser Val Phe Leu Leu Thr Val Pro Phe Arg  
     65             70                 75                 80  
 ttg acc tac ctc atc aag aag act tgg atg ttt ggg ctg ccc ttc tgc      288  
 Leu Thr Tyr Leu Ile Lys Lys Thr Trp Met Phe Gly Leu Pro Phe Cys

85

90

95

aaa ttt gtg agt gcc atg ctg cac atc cac atg tac ctc acg ttc cta	336
Lys Phe Val Ser Ala Met Leu His Ile His Met Tyr Leu Thr Phe Leu	
100 105 110	
ttc tat gtg gtg atc ctg gtc acc aga tac ctc atc ttc ttc aag tgc	384
Phe Tyr Val Val Ile Leu Val Thr Arg Tyr Leu Ile Phe Phe Lys Cys	
115 120 125	
aaa gac aaa gtg gaa ttc tac aga aaa ctg cat gct gtg gct gcc agt	432
Lys Asp Lys Val Glu Phe Tyr Arg Lys Leu His Ala Val Ala Ala Ser	
130 135 140	
gct ggc atg tgg acg ctg gtg att gtc att gtg gta ccc ctg gtt gtc	480
Ala Gly Met Trp Thr Leu Val Ile Val Ile Val Val Pro Leu Val Val	
145 150 155 160	
tcc cgg tat gga atc cat gag gaa tac aat gag gag cac tgc ttt aaa	528
Ser Arg Tyr Gly Ile His Glu Glu Tyr Asn Glu Glu His Cys Phe Lys	
165 170 175	
ttt cac aaa gag ctt gct tac aca tat gtg aaa atc atc aac tat atg	576
Phe His Lys Glu Leu Ala Tyr Thr Tyr Val Lys Ile Ile Asn Tyr Met	
180 185 190	
ata gtc att ttt gtc ata gcc gtt gct gtg att ctg ttg gtc ttc cag	624
Ile Val Ile Phe Val Ile Ala Val Ala Val Ile Leu Leu Val Phe Gln	
195 200 205	
gtc ttc atc att atg ttg atg gtg cag aag cta cgc cac tct tta cta	672
Val Phe Ile Ile Met Leu Met Val Gln Lys Leu Arg His Ser Leu Leu	
210 215 220	
tcc cac cag gag ttc tgg gct cag ctg aaa aac cta ttt ttt ata ggg	720
Ser His Gln Glu Phe Trp Ala Gln Leu Lys Asn Leu Phe Phe Ile Gly	
225 230 235 240	
gtc atc ctt gtt tgc ttc ctt ccc tac cag ttc ttt agg atc tat tac	768
Val Ile Leu Val Cys Phe Leu Pro Tyr Gln Phe Phe Arg Ile Tyr Tyr	
245 250 255	
ttg aat gtt gtg acg cat tcc aat gcc tgc agc agc aag gtt gca ttt	816
Leu Asn Val Val Thr His Ser Asn Ala Cys Ser Ser Lys Val Ala Phe	
260 265 270	
tat aac gaa atc ttc ttg agt gta aca gca att agc tgc tat gat ttg	864
Tyr Asn Glu Ile Phe Leu Ser Val Thr Ala Ile Ser Cys Tyr Asp Leu	
275 280 285	
ctt ctc ttt gtc ttt ggg gga agc cat tgg ttt aag caa aag ata att	912
Leu Leu Phe Val Phe Gly Gly Ser His Trp Phe Lys Gln Lys Ile Ile	
290 295 300	
ggc tta tgg aat tgc gtt ttg tgc cgt	939
Gly Leu Trp Asn Cys Val Leu Cys Arg	
305 310	
<210> 4	
<211> 356	
<212> PRT	
<213> Mus muscalis	
<400> 4	
Met Glu Ile Pro Ala Val Thr Glu Pro Ser Tyr Asn Thr Val Ala Lys	
1 5 10 15	
Asn Asp Phe Met Ser Gly Phe Leu Cys Phe Ser Ile Asn Val Arg Ala	
20 25 30	
Phe Gly Ile Thr Val Pro Thr Pro Leu Tyr Ser Leu Val Phe Ile Ile	

35	40	45		
Gly Val Ile Gly His Val	Leu Val Val Leu Val	Ile Gln His Lys		
50	55	60		
Arg Leu Arg Asn Met	Thr Ser Ile Tyr Leu	Phe Asn Leu Ala Ile Ser		
65	70	75	80	
Asp Leu Val Phe	Leu Ser Thr Leu Pro	Phe Trp Val Asp Tyr Ile Met		
	85	90	95	
Lys Gly Asp Trp	Ile Phe Gly Asn Ala	Met Cys Lys Phe Val Ser Gly		
	100	105	110	
Phe Tyr Tyr	Leu Gly Leu Tyr	Ser Asp Met Phe Phe Ile Thr Leu Leu		
	115	120	125	
Thr Ile Asp Arg Tyr	Leu Ala Val Val His	Val Val Phe Ala Leu Arg		
	130	135	140	
Ala Arg Thr Val Thr	Phe Gly Ile Ile Ser	Ser Ile Ile Thr Trp Val		
	145	150	155	160
Leu Ala Ala Leu Val	Ser Ile Pro Cys	Leu Tyr Val Phe Lys Ser Gln		
	165	170	175	
Met Glu Phe Thr Tyr	His Thr Cys Arg Ala	Ile Leu Pro Arg Lys Ser		
	180	185	190	
Leu Ile Arg Phe Leu Arg	Phe Gln Ala Leu Thr	Met Asn Ile Leu Gly		
	195	200	205	
Leu Ile Leu Pro Leu Leu	Ala Met Ile Ile Cys	Tyr Thr Arg Ile Ile		
	210	215	220	
Asn Val Leu His Arg	Arg Pro Asn Lys	Lys Ala Lys Val Met Arg		
	225	230	235	240
Leu Ile Phe Val Ile	Thr Leu Leu Phe	Phe Leu Leu Ala Pro Tyr		
	245	250	255	
Tyr Leu Ala Ala	Phe Val Ser Ala	Phe Glu Asp Val Leu Phe Thr Pro		
	260	265	270	
Ser Cys Leu Arg Ser	Gln Gln Val Asp	Leu Ser Leu Met Ile Thr Glu		
	275	280	285	
Ala Leu Ala Tyr Thr	His Cys Cys Val Asn	Pro Val Ile Tyr Val Phe		
	290	295	300	
Val Gly Lys Arg Phe	Arg Lys Tyr Leu Trp	Gln Leu Phe Arg Arg His		
	305	310	315	320
Thr Ala Ile Thr Leu	Pro Gln Trp Leu	Pro Phe Leu Ser Glu Asp Arg		
	325	330	335	
Ala Gln Arg Ala Ser	Ala Arg Leu Pro	Ser Thr Val Glu Ile Glu Thr		
	340	345	350	
Ser Ala Asp Leu				
	355			

<210> 5  
 <211> 68  
 <212> PRT  
 <213> Mus muscalis

<400> 5  
 Arg Asn Met Thr Ser Ile Tyr Leu Phe Asn Leu Ala Ile Ser Asp Leu  
 1 5 10 15  
 Val Phe Leu Ser Thr Leu Pro Phe Trp Val Asp Tyr Ile Met Lys Gly  
 20 25 30  
 Asp Trp Ile Phe Gly Asn Ala Met Cys Lys Phe Val Ser Gly Phe Tyr  
 35 40 45  
 Tyr Leu Gly Leu Tyr Ser Asp Met Phe Phe Ile Thr Leu Leu Thr Ile  
 50 55 60  
 Asp Arg Tyr Leu  
 65

<210> 6  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> VARIANT  
 <222> (1)...(1)  
 <223> Xaa at position 1 can be G or S or T or A or  
 L or I or V or M or F or Y or W or C

<221> VARIANT  
<222> (2)...(2)  
<223> Xaa at position 2 can be G or S or T or A or  
N or P or D or E

<221> VARIANT  
<222> (3)...(3)  
<223> Xaa at position 3 can not be E or D or  
P or K or R or H

<223> Xaa at position 4 can  
be any amino acid

<223> Xaa at position 5 can  
be any amino acid

<221> VARIANT  
<222> (6)...(6)  
<223> Xaa at position 6 can be L or I or V or M or  
N or Q or G or A

<223> Xaa at position 7 can  
be any amino acid

<223> Xaa at position 8 can  
be any amino acid

<221> VARIANT  
<222> (9)...(9)  
<223> Xaa at position 9 can be L or I or V or M or  
F or T

<221> VARIANT  
<222> (10)...(10)  
<223> Xaa at position 10 can be G or S or T or A or  
N or C

<221> VARIANT  
<222> (11)...(11)  
<223> Xaa at position 11 can be L or I or V or M  
or F or Y or W or S or T or A or C

<221> VARIANT  
<222> (12)...(12)  
<223> Xaa at position 12 can be D or E or N or H

<221> VARIANT  
<222> (14)...(14)  
<223> Xaa at position 14 can be F or Y or W or C  
or S or H

<223> Xaa at position 15  
can be any amino acid

<223> Xaa at position 16  
can be any amino acid

<221> VARIANT  
<222> (17)...(17)  
<223> Xaa at position 17 can be L or I or V or M

<400> 6  
Xaa Arg Xaa Xaa Xaa  
1 5 10 15  
Xaa